



MPRIMIKGGVWRNTEDEILKAAVMKYGKNQWSRIASLLHRKSAKQCKARW 50
YEWLDPSIKKTEWSREEEEEKLLHLAKLMPTQWRTIAPIIGRTAAQCLEHY 100
EFLLDKAAQRDNEEETTDDPRKLKPGEIDPNPETKPARPDPIDMDEDELE 150
MLSEARARLANTQGKKAKRKAREKQLEEARRLAALQKRRELRAAGIEIQK 200
KRKRKRGV DYN AEIPFEKKPALGFYDTSEENYQALDADFRKLRQQDL DGE 250
LRSEKEGRDRKKDKOHLKRKKESDLPSAILQTSGVSEFTKKRSKLVLPAP 300
QISDAELQEVVKVGQASEIARQTAEESGITNSASSTLLSEYNVTNNSVAL 350
RTPRTPASQDRILQEAQNLMA L TNVDTPLKGG LNTPLHESDFSGVTPQRO 400
VVQTPNTVLSTPFRTPSNGAEG LTPRSGTTPKPVINSTPGRTPLRDKLNI 450
NPEDGMADYSDPSYVKOMERESREHLRLGLLGLPAPKNDFEIVLPENAEK 500
ELEEREIDDTYIEDAADVDARKQAIRDAERVKEMKRMHKAVQKDLPRPSE 550
VNETILRPLNVEPPLTDLQKSEELIKKEMITMLHYDLLHHPYEPSGNKKG 600
KTVGFGTNNSEHITYLEHNPYEKFSKEELKKAQDVLVQEMEVVKQGM SHG 650
ELSSEAYNQVWEECY SQVLYLPGQSR YTRANLASKKDRIESLEKRLEINR 700
GHMTTEAKRAAKMEKKMKILLGGYQSRAMGLMKQLNDLWDQIEQAHL ELR 750
TFEELKKHEDSAIPRRLECLKEDVQRQQEREKELQHRYADLLLEKETLKS 800

KF*

Fig. 1A

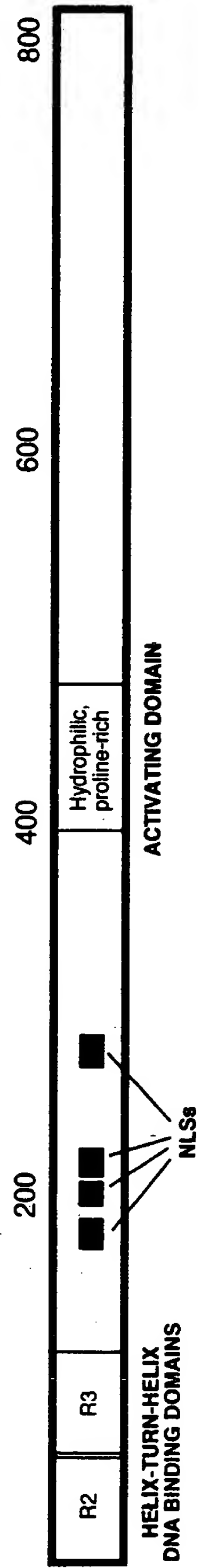


Fig. 1B

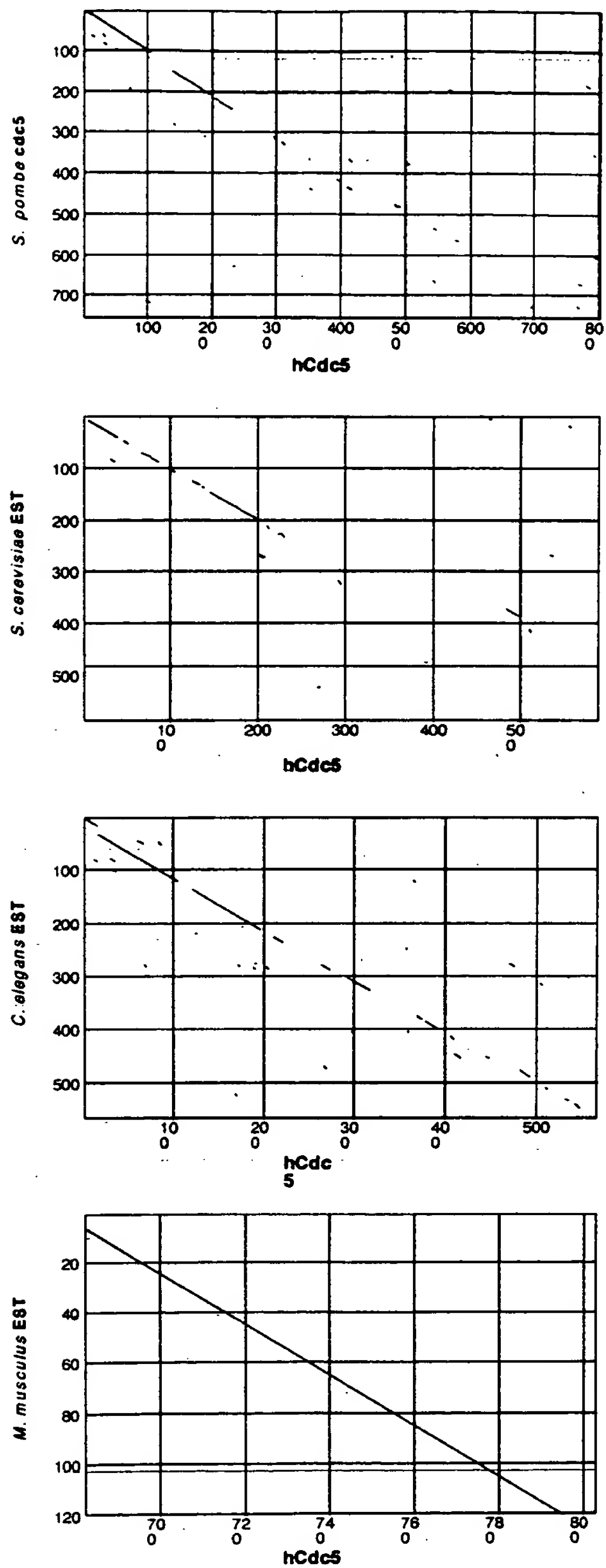


Fig. 2A

Fig. 2B



hCdc5	PLKGGNTPLHESDFSGVTPQRQVVQTPNTVLSTPFRTPSNGAEGLTPRS GTTPKPVINSTP (378-439)
<i>S. pombe</i> cdc5	SVTIEVRNQLMNREQSSLLGQESIPLQPGGTGYTGVT-PSHAANGS---ALAAP--Q--ATP (380-434)
b-Myb	PVK-TL--PFSPSQFLNFWNKQDTLEESPSLTSTPVC SQKVVTTPPLHRDKTPLHQKHAAF (445-503)
a-Myb	ILRKKRMRVGHSPGSEL-RDGSUNDGGNMALKTPLKTPFSPSQFFNTCPGNEQLNIENPSF (446-508)

hCdc5	GRTPLRDKLININREDGMADYSDPSYVKQMERESREHLRLGLGLPAPKNDFEIVLPENAEK (440-500)
<i>S. pombe</i> cdc5	FRTPR-DTFSINAAERAGR-LASE-REN-KIRLKALRELLAKLPKPKNDYEL-ME-P-R- (435-487)
b-Myb	VTPDQKYSMDNTPHTP-TPFKNAKYGPKLPQTPHLEEDLKEVLRSEAGIELIIEDDIRP (504-565)
a-Myb	TSTPICGQKAL-ITTPLHKETTPKQDKENVGFRPTIRR SILGTPRTPTPFKNALAAQEKK (509-569)

Fig. 2C



5' untranslated region:

GGCAGGAGAGGAAGTGGCGGCTTTGAGTCCGGTGGCCCAATCGCTGTTACTACTTCTCTGAAGCTCCTCTCGGCTGCTTGC
CGAGACACCTTGGCCCAAG

Coding region:

1 DNA BINDING DOMAIN (___)
1 atgcccgcgaa ttatgatcaa ggggggcgta tggaggaata ccgaggaratg aattctgaaa
61 gcagcggtaa tgaatatatg gaaaaatcag tggctcagga ttgcctcatt gctgcataga
121 aaatcagcaa agcagtgcaa agccagatgg tatgaatggc tggatccaaq cattaaagaq
181 acagaatggc ccagagaaga agaggaaaaa ctcttgcaat tggccaaqct gatgccaaat
241 cagtcgagga ccattgctcc aatcattgga agaacagcgg cccagtgctt agaacactat
301 gaatttcttc tggataaaagc tgcccaaaga gacaatgaag aggaacaac agatgatcca
361 cgaaaactta aacctggaga aatagatcca aatccagaaa caaaaccagc gcggcctgat
421 ccaattgata tggatgagga tgaacttgag atgctttctg aagccagagc ccgcttggct
2 NUCLEAR LOCALIZATION DOMAIN (....)
481 aatactcagg gaaagaaggc caagaggaaa gcaagagaga aacaattgga agaagcaaga
541 cgtcttgctg ccctccaaaa aagaagagaa cttcgagcag ctggcataga aattcagaag
601 aaaagaaaaa ggaagagagg agttgattat aatgccgaaa tcccatttga aaaaaagcct
661 gcccttggtt tttatgatac ttctgaggaa aactaccaag ctcttgacgc agatttcagg
721 aaattaagac aacaggatct tgaatggggag ctaagatctg aaaaagaagg aagagataga
781 aaaaaagaca aacagcattt gaaaaggaaa aaagaatctg atttaccatc agctattctt
841 caaactagtg gtgtttctga atttactaaa aagagaagca aactagtact tcctgccctt
901 cagatttcag atgcagaact ccaggaagtt gtaaaagtag gccaaagcag tgaatttga
961 cgtcaaactg ccgaggaatc tggcataaca aattctgctt ccagtacact tttgtctgag
1021 tacaatgtca ccaacaacag cgttgctctt agaacaccac gaacaccagc ttcccaggac
1081 agaattctgc aggaagccca gaacctcatg gccctcacca atgtggacac cccattgaaa
3 ACTIVATING DOMAIN (___)
1141 ggtggactta ataccctatt gcattgagat gacttctcag gtgtaactcc acagcgacaa
1201 gttgatcaga ctccaaacac agttctctct actccattca ggaactcctt taatggagct
1261 gaagggctga ctccccggag tggaaacaact cccaaccag ttattaactc tactccgggt
1321 agaactcctc ttccagacaa gttaaacatt aatcccagag atggaatggc agactatagt
1381 gatccctctt acgtgaagca gatggaaaga gaatcccag aacatctccg tttaggggtg
1441 ttgggccttc ctgcccctaa gaatgatttt gaaattgttc taccagaaaa tgccgagaag
1501 gagctggaag aacgtgaaat agatgatact tacattgaag atgctgctga tgtggatgct
1561 cgaaagcagg ccatacgaga tgcagagcgt gtaaaggaaa tgaacgaat gcataaagct
1621 gtccagaaag atctgccaa accatcagaa gtaaatgaaa ctattctaag acccttaa
1681 gtagaaccgc ctttaacaga ttacagaaa agtgaagaac taatcaaaaa agaatgatc
1741 acaatgcttc attatgacct tctacatcac ccttatgaac catctggaaa taaaaaaggc
1801 aaaactgtag ggtttggtac caataattca gagcacatta cctatctgga acataatcct
1861 tatgaaaagt tctccaaaga agagctgaaa aaggcccagg atgttttggg gcaggagatg
1921 gaagtgggta aacaagggaat gagccatgga gagctctcaa gtgaagctta taaccagggtg
1981 tgggaagaat gctacagtca agttttatat ctctctgggc agagccgcta cacacggg
2041 aatctggcta gtaaaaagga cagaattgaa tcacttgaaa agaggctcga gataaacagg
2101 ggtcacatga cgacagaagc caagagggct gcaaagatgg aaaagaagat gaaaattttg
2161 cttgggggtt accagtctcg tgctatgggg ctcatgaaac agttgaatga cttatgggac
2221 caaattgaac aggctcactt ggagttacgc acttttgaag aactcaagaa acatgaagat
2281 tctgctattc ccggaggct agagtgtcta aaagaagacg ttcagcgaca acaagaaaga
2341 gaaaaggaac ttcaacatag atatgctgat ttgctgctgg agaaagagac tttaaagtca
2401 aaattctga

untranslated region:

AGTACAGTTTATATCTGTACAGGATTAATTAATGCGGTTTTTCATACTCTAGAAAGCTGAAACTG ATGTTTATCTTCATTGACA
AATTTACCCACCATCTGTGTTTTTCAGTTGTTTTATTTTAAATGATATCGATCTTACACATCTGTGTATAAAGACCTTAACCTCACA
GGACGGACATTTTAGAGTTTAAATTATTA AGGCTATCATCTCTTTAGTAAATGTCATATTTGCCAACTTTTTTAGTTTTGGCCTTTAA
TTTAAAAGCCTAATTTTAAAGTGCTGCTGTGAGTAACTCTTGAATAAAAACAAATATAAAAA

Fig. 2D

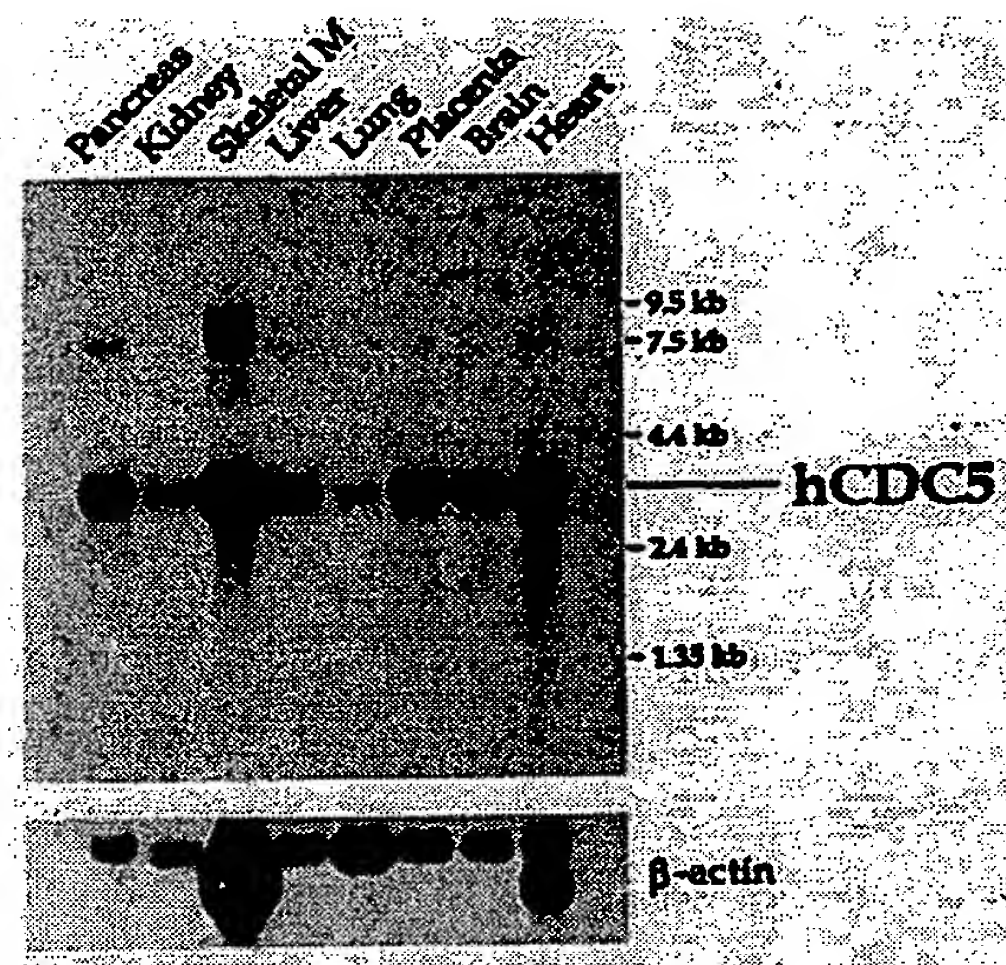


FIG. 3

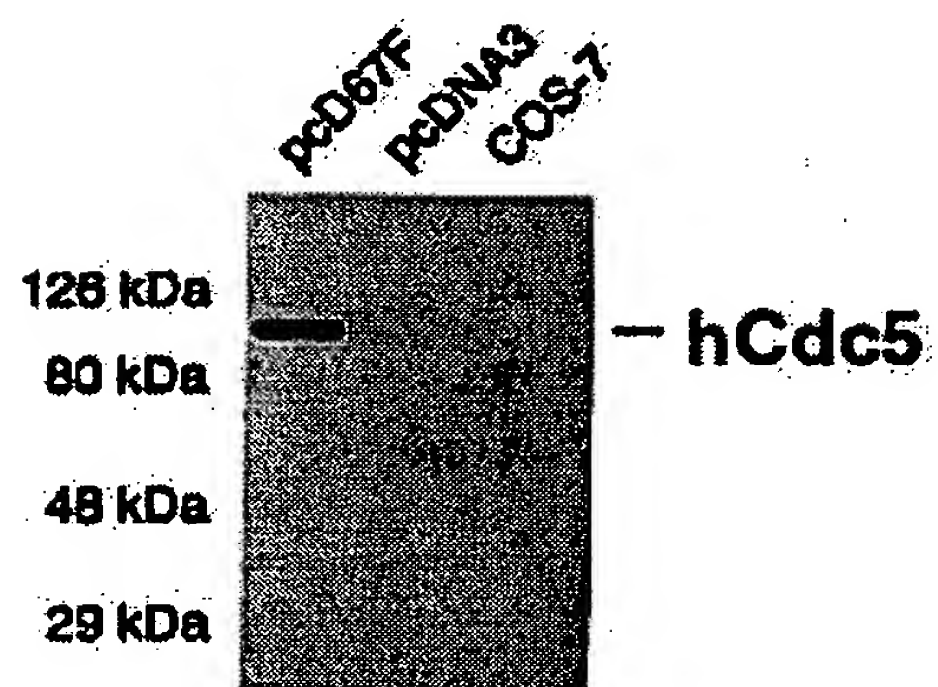


FIG. 4A

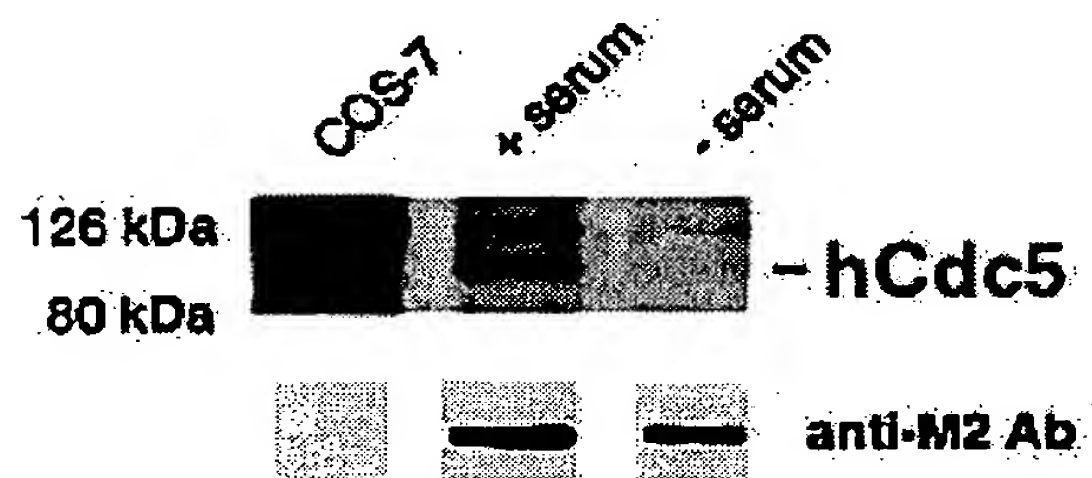


FIG. 4B

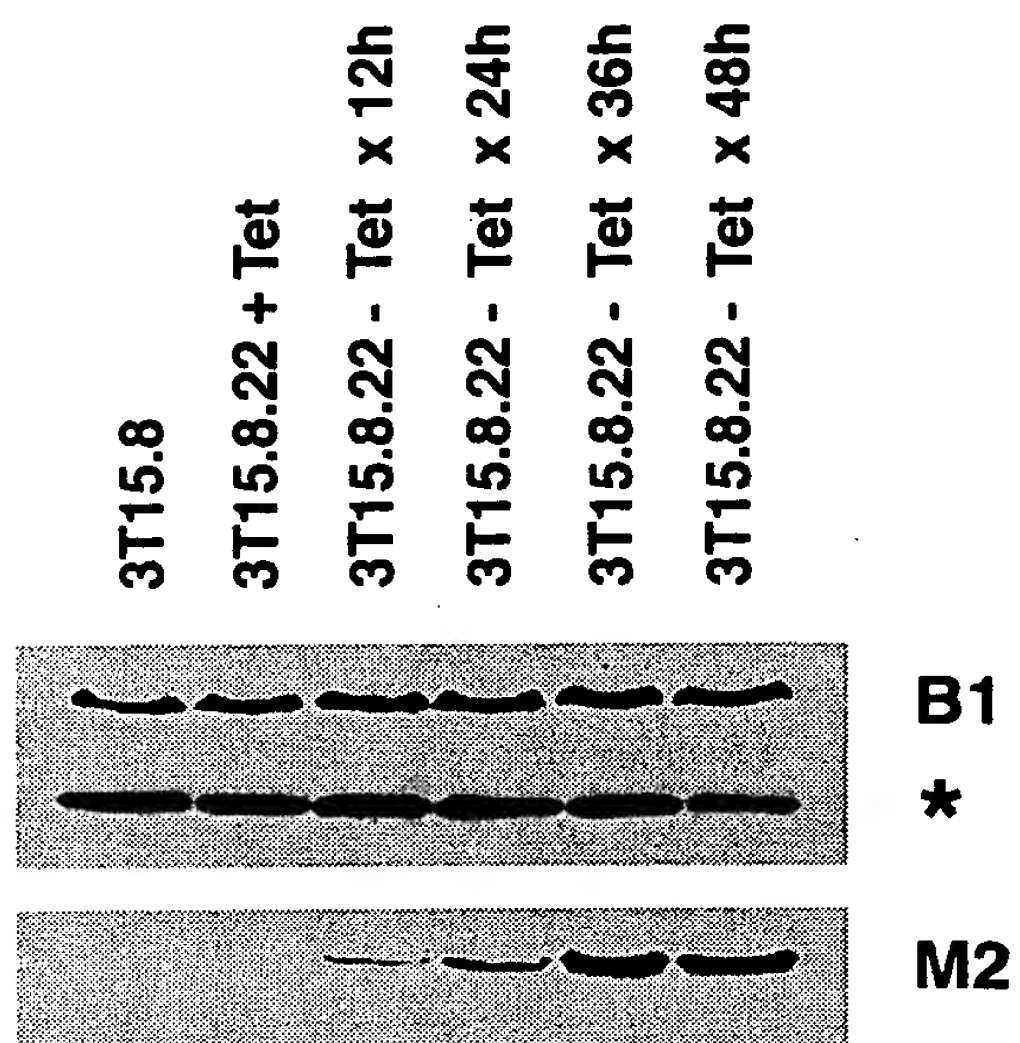


FIG. 5

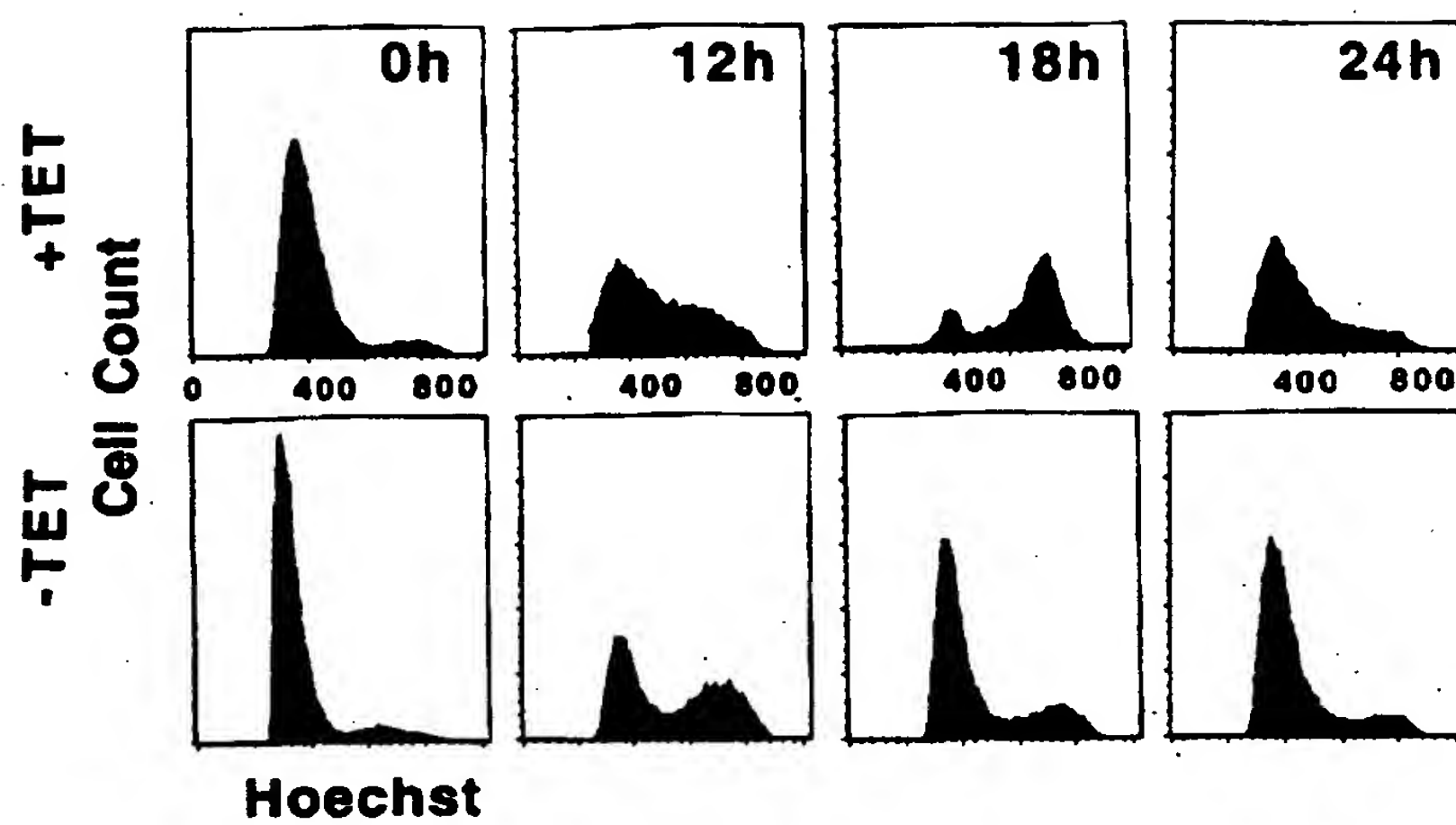


Fig. 6

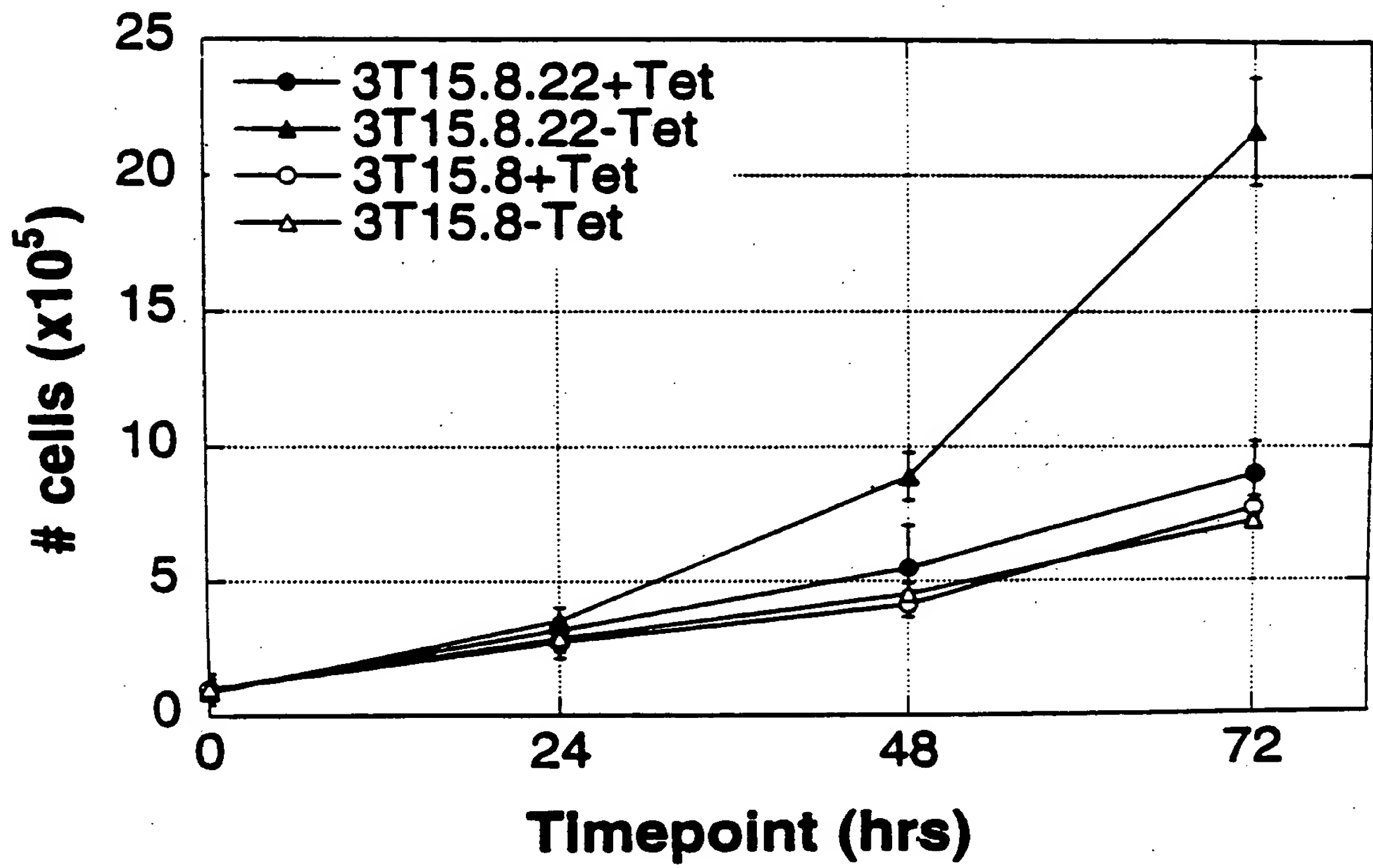
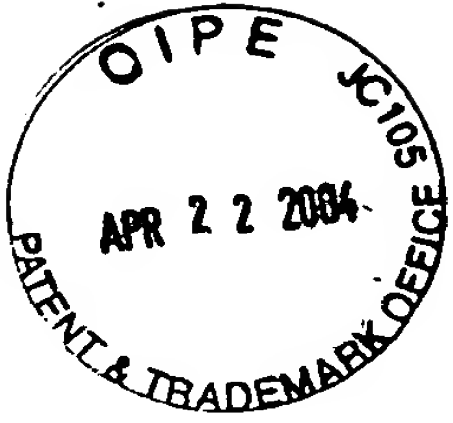


Fig. 7

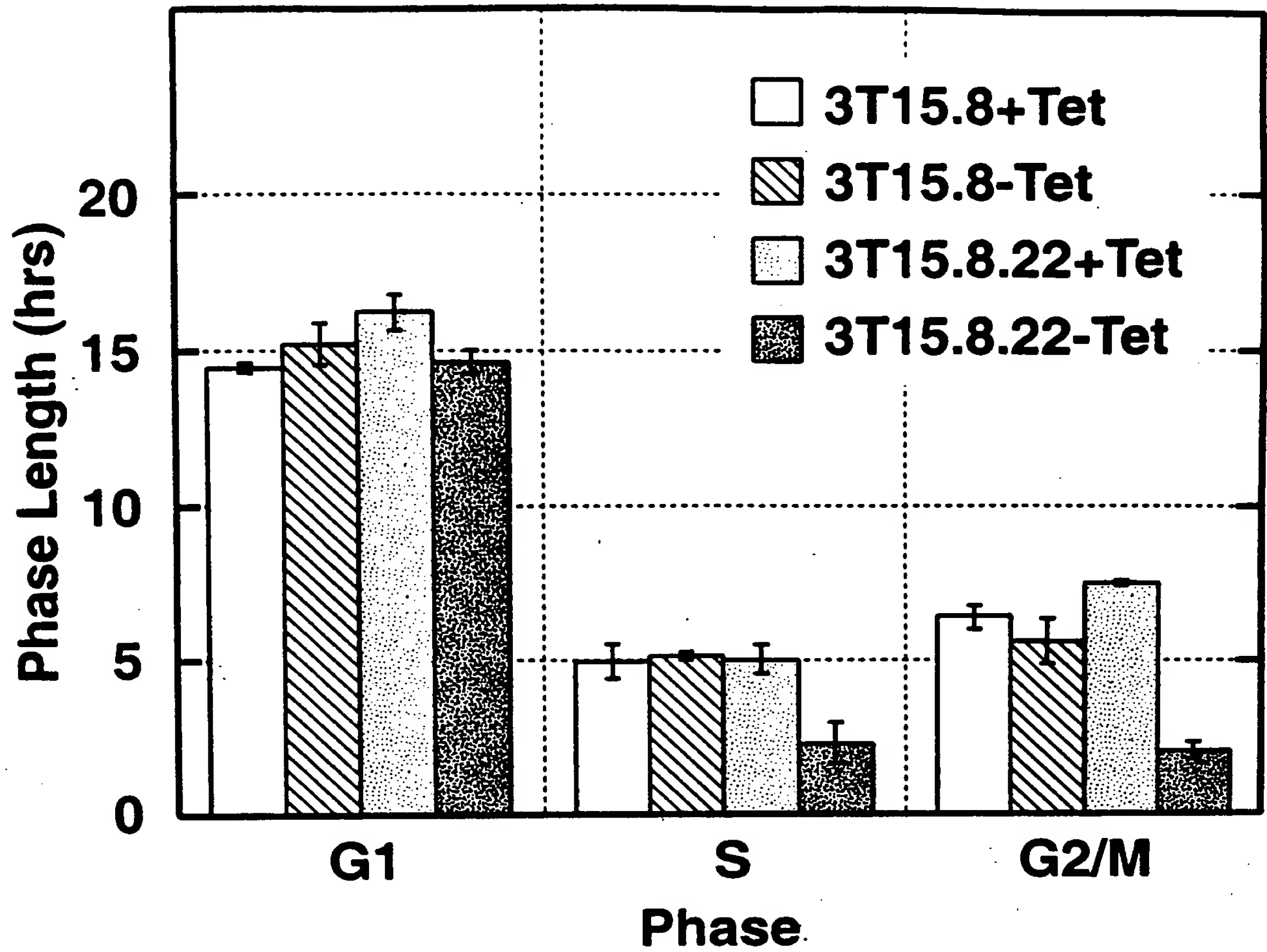


FIG. 8

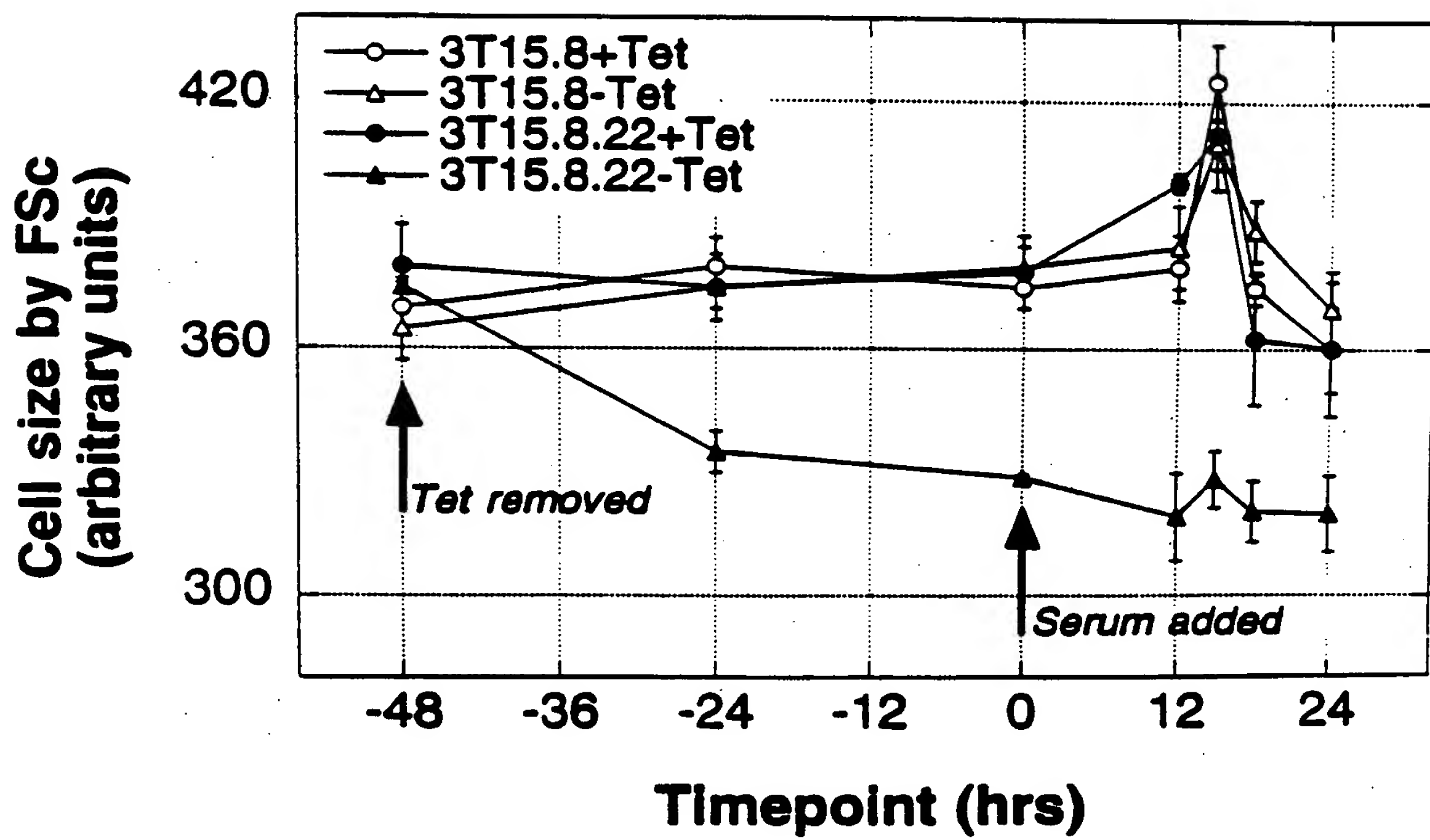
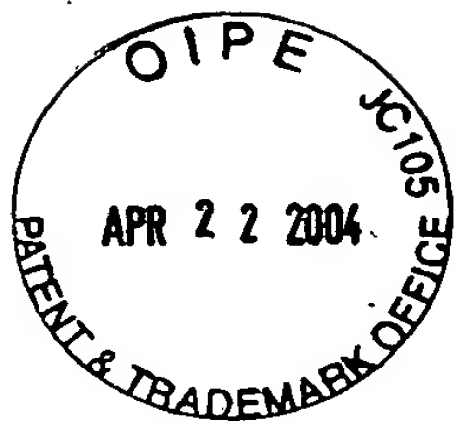


Fig. 9

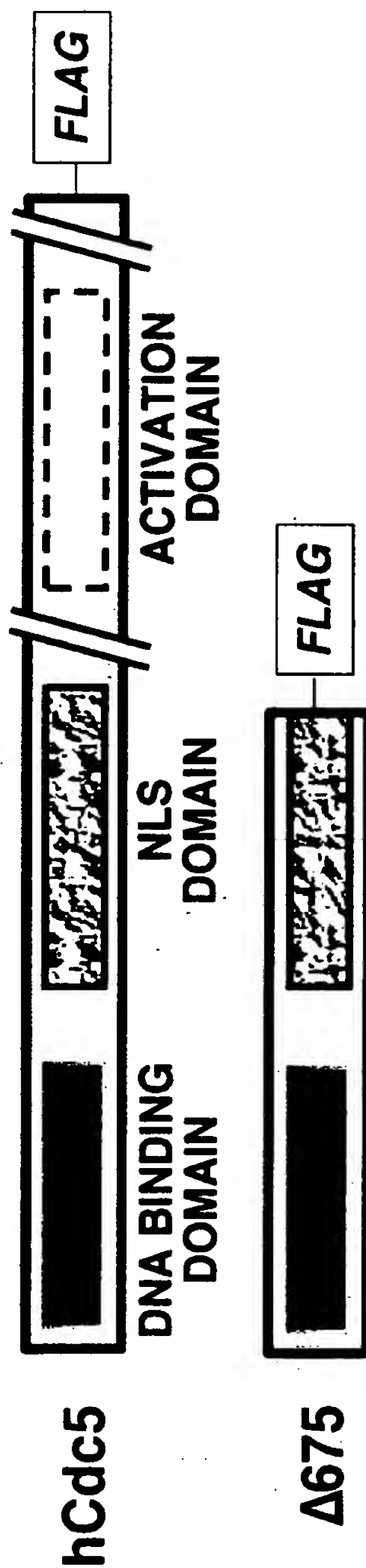
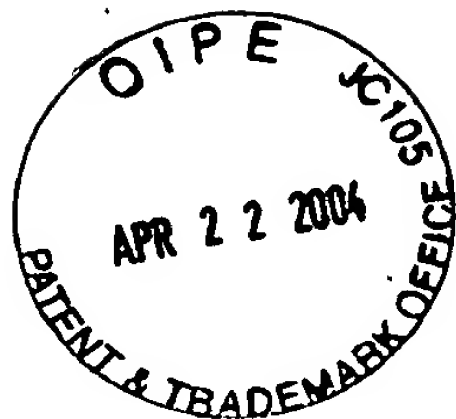


Fig. 10

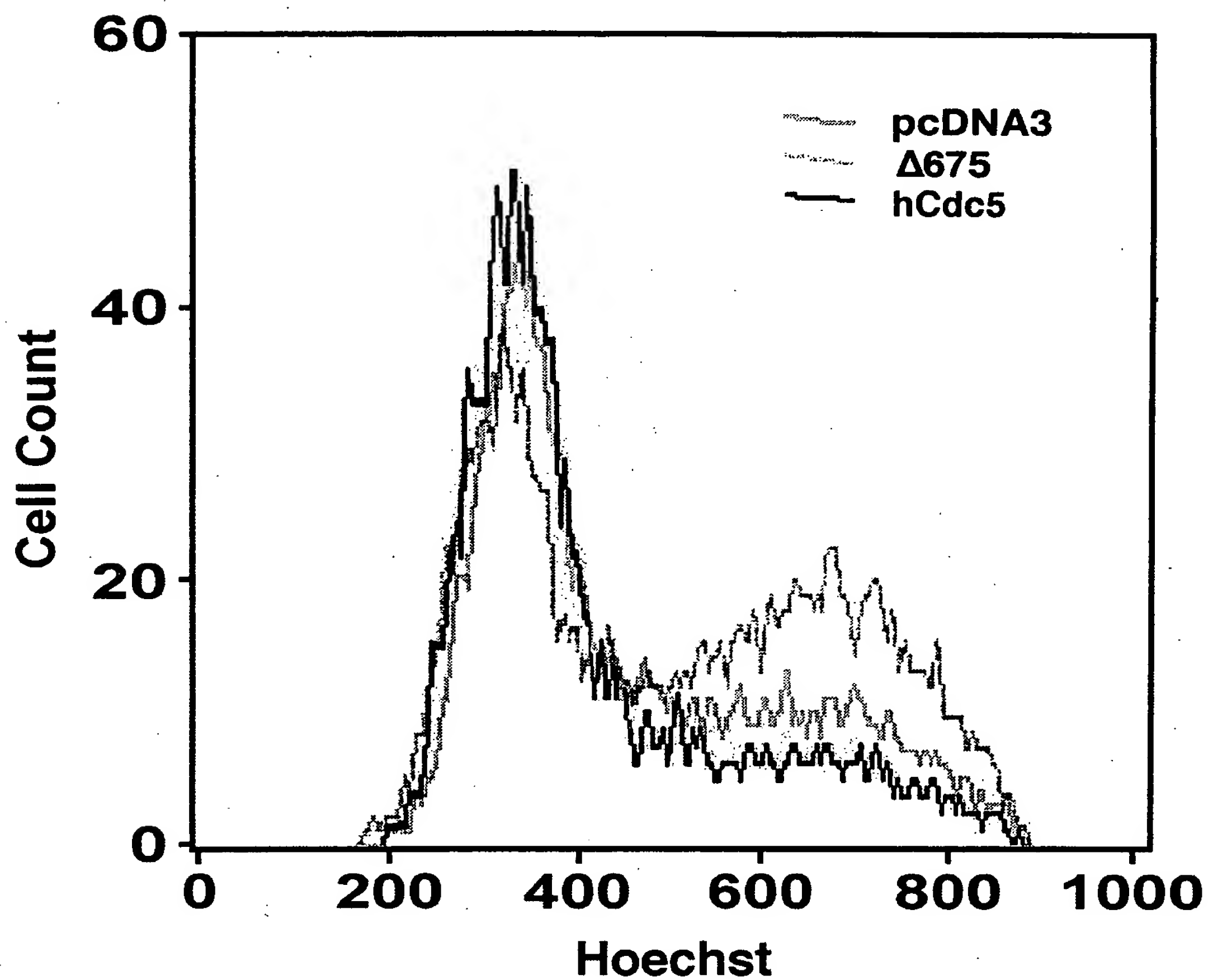


FIG. 11

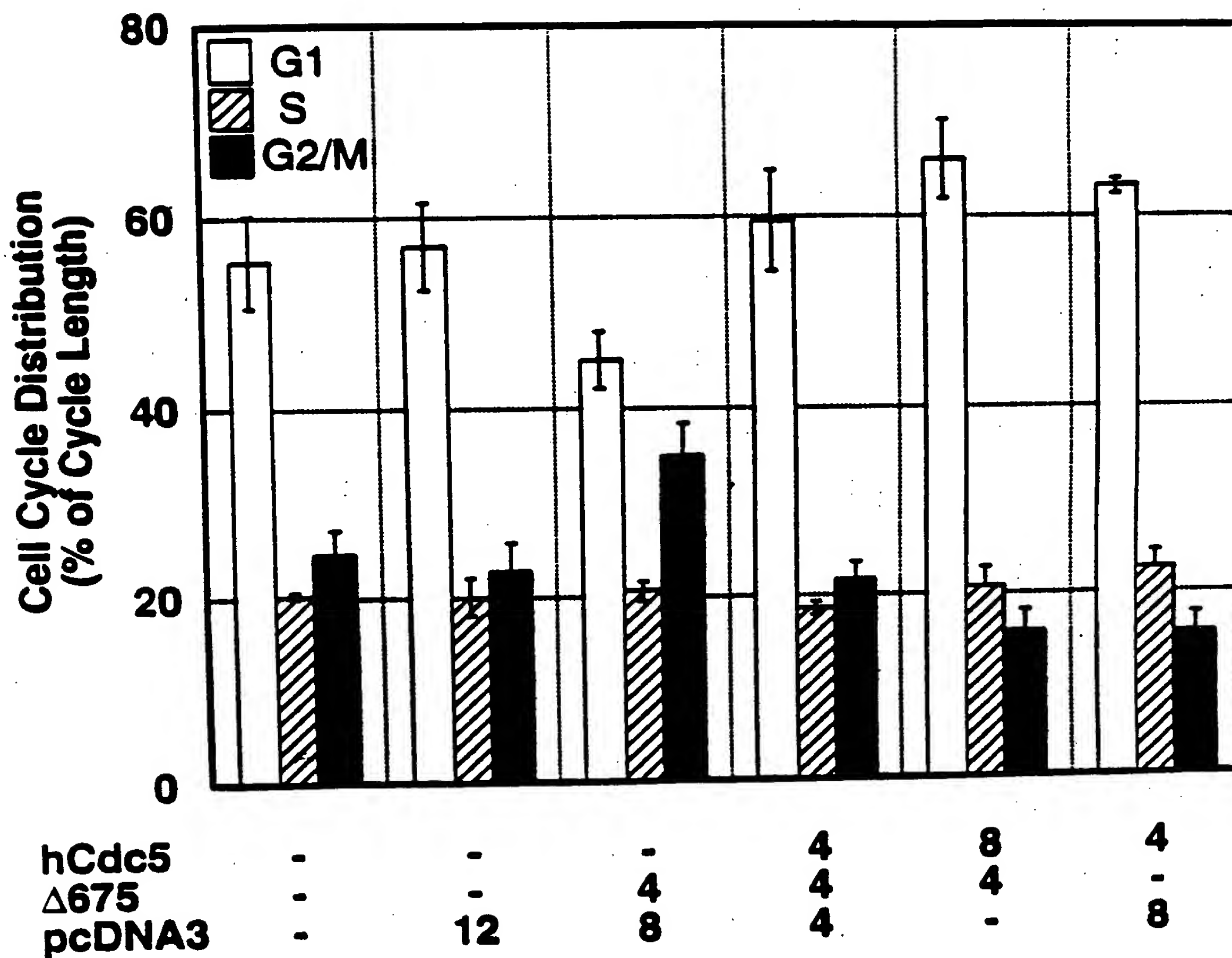


Fig. 12

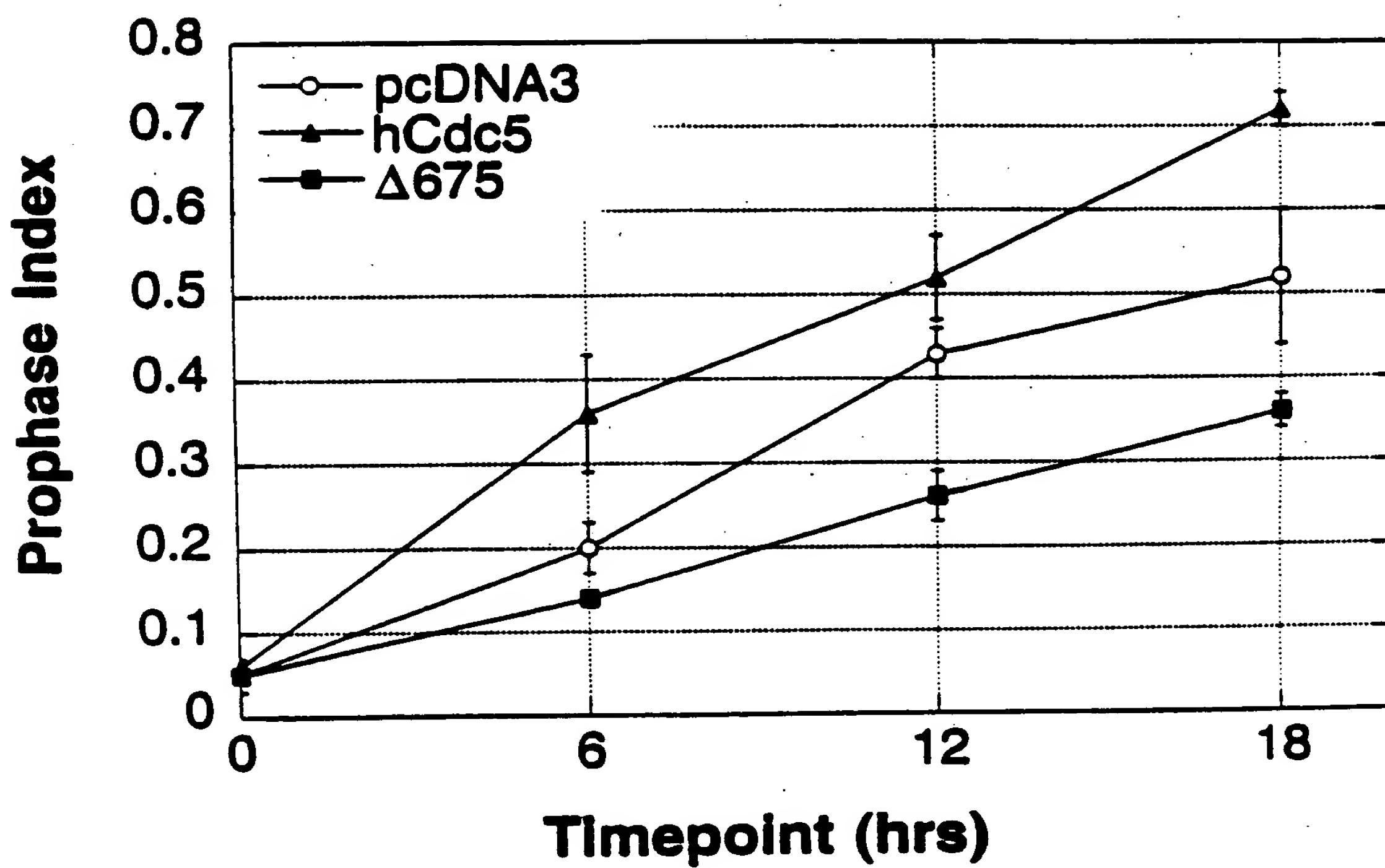
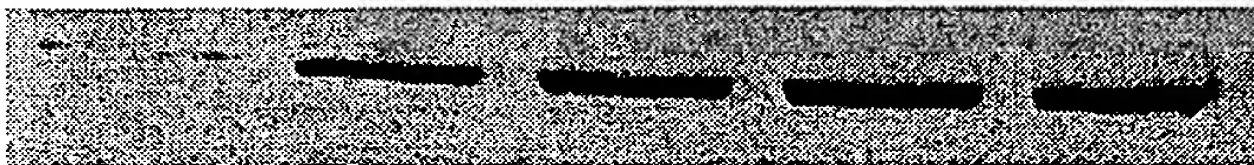


Fig. 13



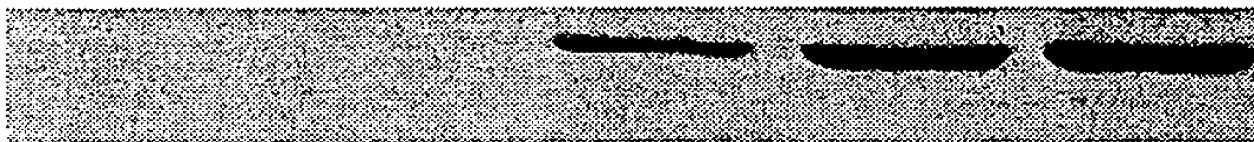
0 12 15 18 21 hrs



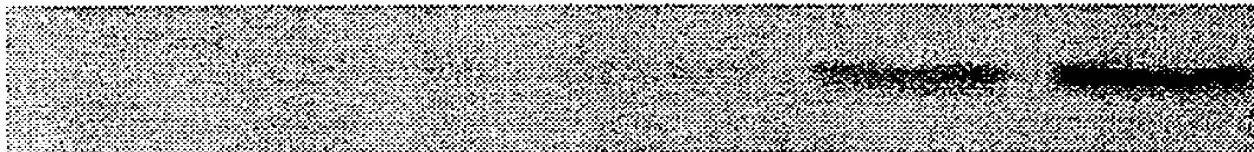
hCdc5



p50 CLNE



p60 CLNA



p62 CLNB1

FIG. 14A

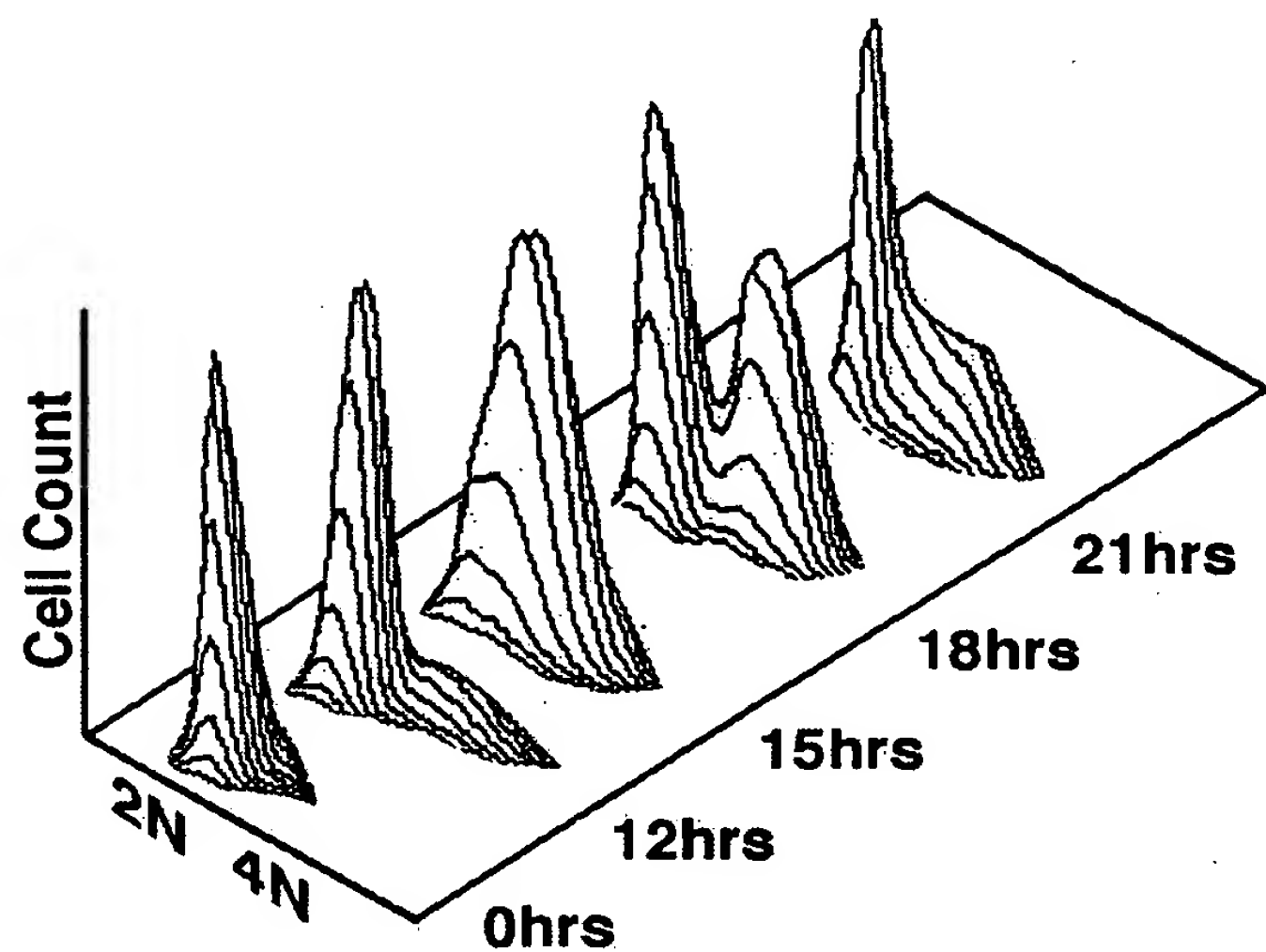


FIG. 14B



Consensus

G A T T T A A C A T A A

(SEQ ID NO:13)

8.05

G A T T T A A C A T A A

8.04

G A T T T A A C A T A A

8.03

G A T T T A A C A T A A

8.02

G A T T T A A C A T A A

8.01

G A T T T A A C A T A A

6.05

G G T G T A A C G T G G

(SEQ ID NO:36)

6.04

G T G T T A C C A C A T

(SEQ ID NO:37)

6.03

C C A T A A A T T T A G

(SEQ ID NO:38)

6.02

G A G A T A A A G T C T

(SEQ ID NO:39)

6.01

G T G T T A T T G A A A

(SEQ ID NO:40)

3.05

A C C C A C G T C T A T

(SEQ ID NO:41)

3.04

G G T T A G G A T A G G

(SEQ ID NO:42)

3.03

G T T G A G T A G T A T

(SEQ ID NO:43)

3.02

C T G T T A A T T T C C

(SEQ ID NO:44)

3.01

G G T G T T A T T G A T

(SEQ ID NO:45)

FIG 15